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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/855,750

DATE: 09/18/2001

TIME: 16:03:32

Input Set : A:\032301W1181.seq.ST25.txt

Output Set: N:\CRF3\09182001\I855750.raw

3 <110> APPLICANT: Nampoothiri, Madhavan K.
5 <120> TITLE OF INVENTION: Nucleotide Sequences Which Code For The fadD15 Gene
7 <130> FILE REFERENCE: 032301 WD 1181
9 <140> CURRENT APPLICATION NUMBER: 09/855,750
C--> 10 <141> CURRENT FILING DATE: 2001-08-31
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2300
18 <212> TYPE: DNA
19 <213> ORGANISM: Corynebacterium glutamicum
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23 <222> LOCATION: (247)..(2103)
24 <223> OTHER INFORMATION:
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28 <221> NAME/KEY: -10_signal
29 <222> LOCATION: (95)..(100)
30 <223> OTHER INFORMATION:
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39 <220> FEATURE:
40 <221> NAME/KEY: RBS
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48 aaatacatct tttggattgg gctttgggggt ggcttttata caccctgatt ggtgcagata 120
50 taagaagtta ttgacacact gaatacatag agaaaaattc catgtgggta aagatatgcc 180
52 taaagatctg accaaaaacg tgactaaaga cgtgacgaca caagtacagc caaattaaag 240
54 gaaagg ttg aat ttg acc atg act tca cct aat acc ctg cag gaa tac 288
55 Leu Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr
56 1 5 10
58 act gaa cct gcc aag tac acc atc gga gaa tct gaa acc tgc ctg acc 336
59 Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr
60 15 20 25 30
62 gcc ctt cta gat cag att aag act cga cct tac gga gtt ttg ttc agc 384
63 Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser
64 35 40 45
66 aag cct gcc aac tat gag tgg gtg aat gta act gcc aaa gaa ttt cag 432
67 Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln
68 50 55 60
70 gac gag gtt ttt gcg gtt gca aaa gga att att tca gtc ggc gta gag 480
71 Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu
72 65 70 75

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74  cag gga gac cgt gtc gcg ctg ctg tcc aat act cgc tat gag tgg gct      528
75  Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala
76      80                      85                      90
78  gtg ctt gat ttc gct atc tgg gcc gct ggc gca gtg agc gtg cct atc      576
79  Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile
80  95                      100                      105                      110
82  tac agc tcc tct tca ctg tcc caa att gag tgg atc att gag gat tcc      624
83  Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser
84      115                      120                      125
86  ggc gct gtt ttg gcc att acc gaa acc cct gat cat acc gac ttg atg      672
87  Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met
88      130                      135                      140
90  aag aac ctg gtc atc ggt gaa gac gga act cca gcg att aag ggt tca      720
91  Lys Asn Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser
92      145                      150                      155
94  cct tcc aag ctg cgc cgc att cta gag atc aac tct tcg gcg ttg gag      768
95  Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu
96      160                      165                      170
98  acc ttg aag ttt gag ggc cgc gag ctt tct gat gag ctg gtg tgg gaa      816
99  Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu
100 175                      180                      185                      190
102 cgc att cat gca acc aag gcc gct gac ctg gcg tct ttg gtg tac acc      864
103 Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr
104      195                      200                      205
106 tct ggc aca act ggt agg ccg aag ggc tgc gag ttg tcc cac tac cac      912
107 Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His
108      210                      215                      220
110 tgg ttg gct gag gtc cga gcg ctg atc acc aat gac atc gga gcg atc      960
111 Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile
112      225                      230                      235
114 gcg atg cca ggt tca agg ttg ctc acc ttc ctt cct ttg gcg cac gtt      1008
115 Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val
116      240                      245                      250
118 ctt gct cgc gca gtg cac ttg gcc ttc gct gtc acc ggt gca acc cag      1056
119 Leu Ala Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln
120 255                      260                      265                      270
122 tcc cac tgg tct gat ttc agc acc ctt act ttg gaa ctg cag cgt tcc      1104
123 Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser
124      275                      280                      285
126 cgc ccg aac ctg att ttg ggt gtt cca cgc gtg ttt gaa aag gtc cgc      1152
127 Arg Pro Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg
128      290                      295                      300
130 aac gcc gct gct gct aat gct gct gac ggt ggc gca atc aag cgc atc      1200
131 Asn Ala Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile
132      305                      310                      315
134 atg ttt gag cgt gcc gaa aag gcg gcc att gaa tac tcc atg gct ctt      1248
135 Met Phe Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu
136      320                      325                      330
138 gat act gca gaa ggc cca agc aag tcc cag gtt atg gca cat aaa gcg      1296

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139 Asp Thr Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala
140 335                               340                               345                               350
142 ttt gac aag ctg gtg tac tcc aag atc cgt gca gct gtc ggt ggc gat      1344
143 Phe Asp Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp
144                               355                               360                               365
146 gtg cag tac gcc atc acc ggt ggt tca gcg atg ggg cag gag ctg ctg      1392
147 Val Gln Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu
148                               370                               375                               380
150 cac ttc ttc cgc ggt gtg ggc atg acc atc tac gaa ggt tat ggt ctg      1440
151 His Phe Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu
152                               385                               390                               395
154 acg gaa tct gcg gct gct gca gcg gtg gac ttc act gat caa aag atc      1488
155 Thr Glu Ser Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile
156 400                               405                               410
158 ggc act gtg ggt aag ccg atg ggt ggc atg acc atc aag atc aat gaa      1536
159 Gly Thr Val Gly Lys Pro Met Gly Gly Met Thr Ile Lys Ile Asn Glu
160 415                               420                               425                               430
162 gat ggc gaa atc atg cta aaa ggc gag atg ttg ttc cag gga tat tgg      1584
163 Asp Gly Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp
164                               435                               440                               445
166 aac aac cca gaa gcc aca gca gaa gcc ctc cac gac ggt tgg ttc aac      1632
167 Asn Asn Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn
168                               450                               455                               460
170 acc ggc gat ctg ggt gag ctg ttg gag tct gga cac ctg gtg atc acc      1680
171 Thr Gly Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr
172                               465                               470                               475
174 gga cgt aag aaa gat ctg atc gtg acc gcg ggc ggc aag aac gtt tcc      1728
175 Gly Arg Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser
176 480                               485                               490
178 cca gga ccc atg gaa gac atc atc cgc gca cac cca ctg gtc agc cag      1776
179 Pro Gly Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln
180 495                               500                               505                               510
182 gcc atg gtg gtg ggc gat ggt aaa cca ttc gtt ggc ctg ctg gtg acc      1824
183 Ala Met Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr
184                               515                               520                               525
186 ttg gat cca gat atg ttg aag cgg tgg aag ctg aac cac aac att gcg      1872
187 Leu Asp Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala
188                               530                               535                               540
190 gaa tcc cgc acg gtt tct gag att gct act gat cct gca ctg cgt gcg      1920
191 Glu Ser Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala
192                               545                               550                               555
194 gaa atc cag gat gca gtc aac aac gct aat gcc acg gtg tct cat tca      1968
195 Glu Ile Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser
196 560                               565                               570
198 gag gcg atc aag cgg ttc tac atc ctt gat cgc gac ctg acc gag gaa      2016
199 Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu
200 575                               580                               585                               590
202 gcc gac gag ctg acc cca acg ctg aag gtc aag cgc aac gtt gtt gtt      2064
203 Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val

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204          595          600          605
206 cgc cgt tac gca gac gcc atc gac cac atc tac aac cga tgagtaacac      2113
207 Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
208          610          615
210 agagacccaa tttgattggg atggatcgac atggacccgc accgaagtcg gcgaagcacc      2173
212 aacacgcttc gctgtgggcg tgatggagga ttgcgcctac attgcagcca ctggcacgga      2233
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221 <212> TYPE: PRT
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224 <400> SEQUENCE: 2
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231          20          25          30
234 Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser Lys Pro
235          35          40          45
238 Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu
239          50          55          60
242 Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly
243 65          70          75          80
246 Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu
247          85          90          95
250 Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser
251          100          105          110
254 Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala
255          115          120          125
258 Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn
259          130          135          140
262 Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser
263 145          150          155          160
266 Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu
267          165          170          175
270 Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu Arg Ile
271          180          185          190
274 His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr Ser Gly
275          195          200          205
278 Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His Trp Leu
279          210          215          220
282 Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile Ala Met
283 225          230          235          240
286 Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val Leu Ala
287          245          250          255
290 Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln Ser His
291          260          265          270
294 Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser Arg Pro
295          275          280          285

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298 Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg Asn Ala
299      290      295      300
302 Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile Met Phe
303 305      310      315      320
306 Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu Asp Thr
307      325      330      335
310 Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala Phe Asp
311      340      345      350
314 Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp Val Gln
315      355      360      365
318 Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu His Phe
319      370      375      380
322 Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu Thr Glu
323 385      390      395      400
326 Ser Ala Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile Gly Thr
327      405      410      415
330 Val Gly Lys Pro Met Gly Gly Met Thr Ile Lys Ile Asn Glu Asp Gly
331      420      425      430
334 Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp Asn Asn
335      435      440      445
338 Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn Thr Gly
339      450      455      460
342 Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr Gly Arg
343 465      470      475      480
346 Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser Pro Gly
347      485      490      495
350 Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln Ala Met
351      500      505      510
354 Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp
355      515      520      525
358 Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser
359      530      535      540
362 Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile
363 545      550      555      560
366 Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala
367      565      570      575
370 Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp
371      580      585      590
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379      610      615
382 <210> SEQ ID NO: 3
383 <211> LENGTH: 24
384 <212> TYPE: DNA
385 <213> ORGANISM: Corynebacterium glutamicum
387 <400> SEQUENCE: 3
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391 <210> SEQ ID NO: 4

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VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date